

Fig. 1

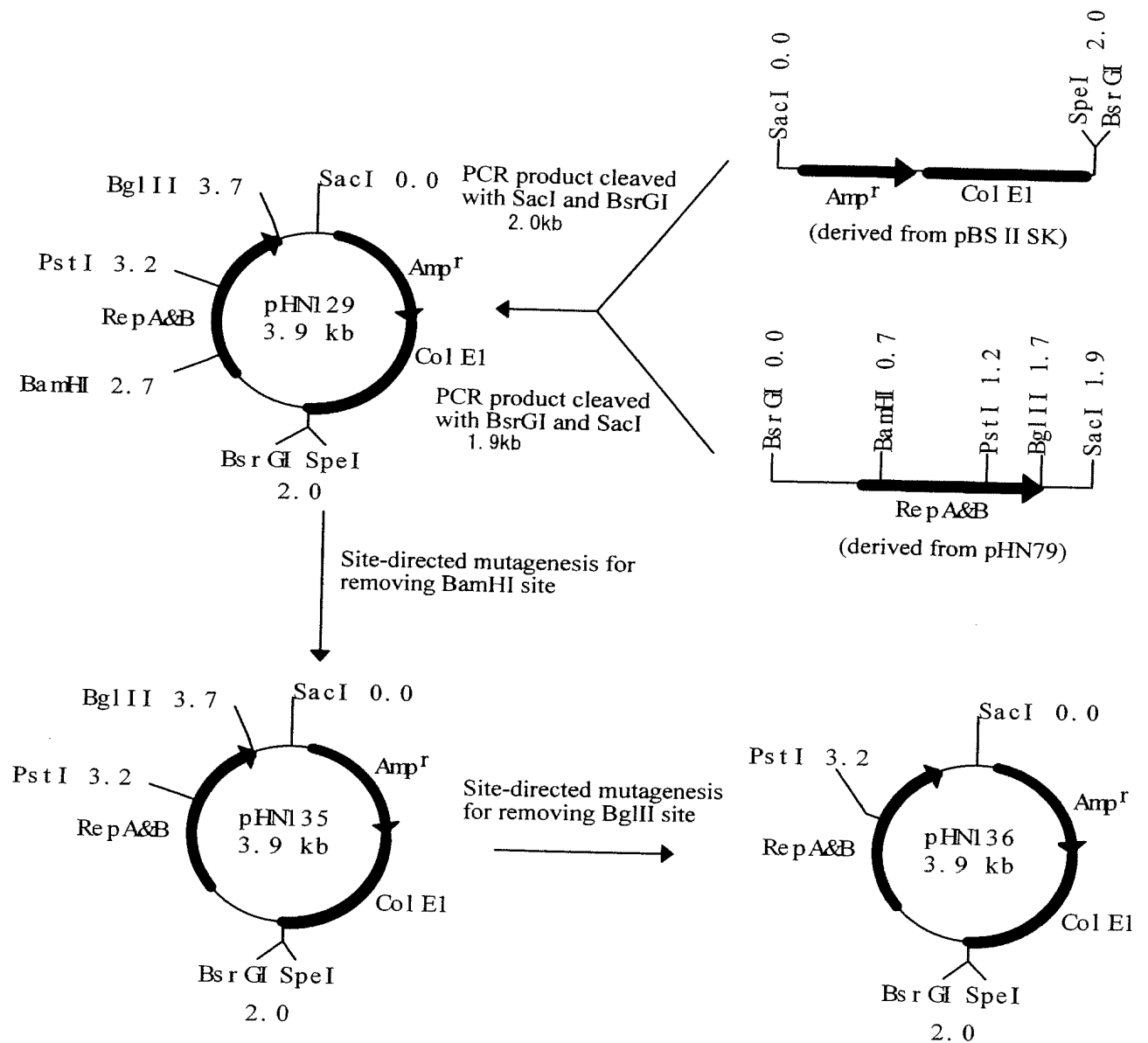


Fig. 2

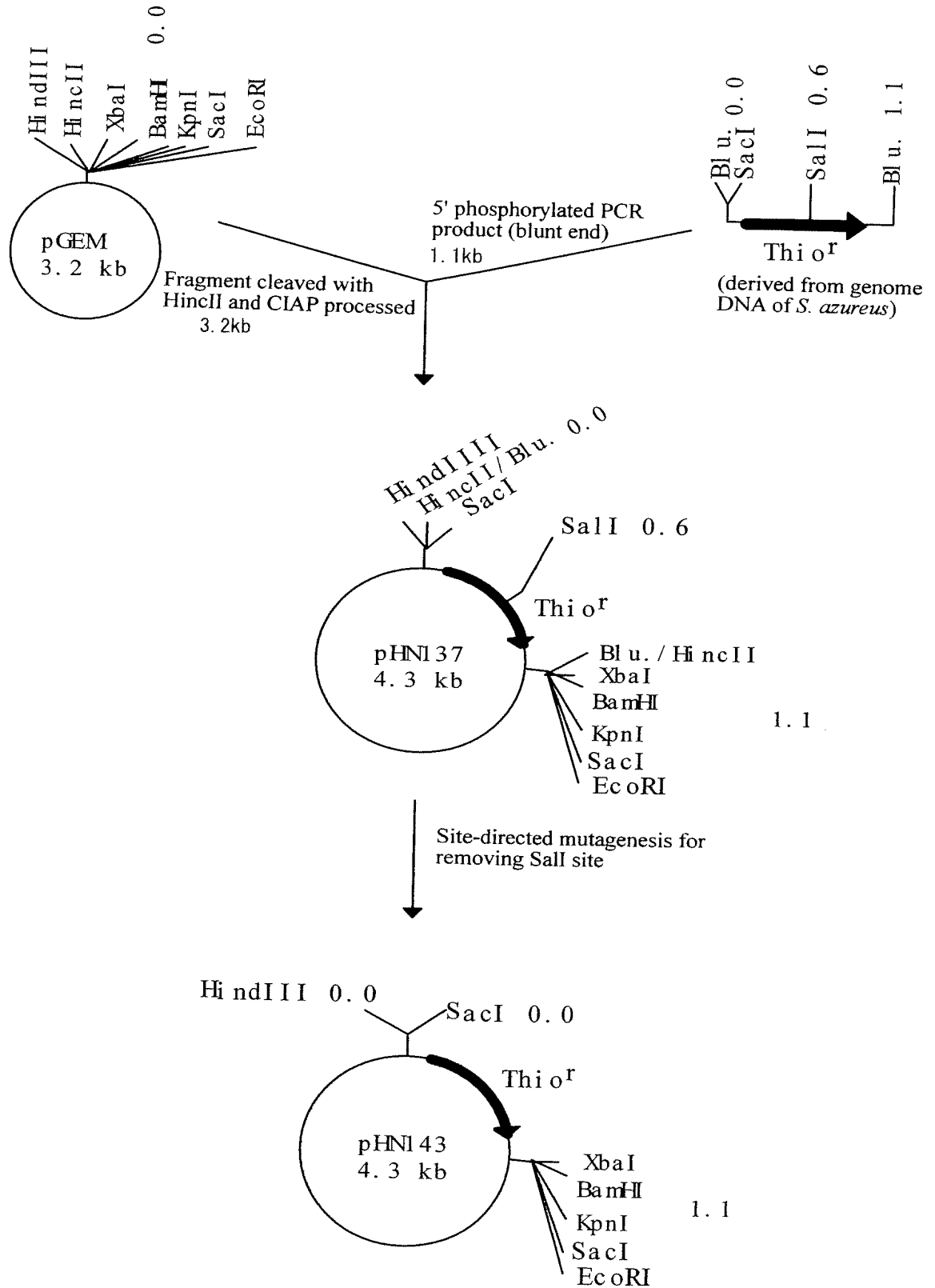


Fig. 3

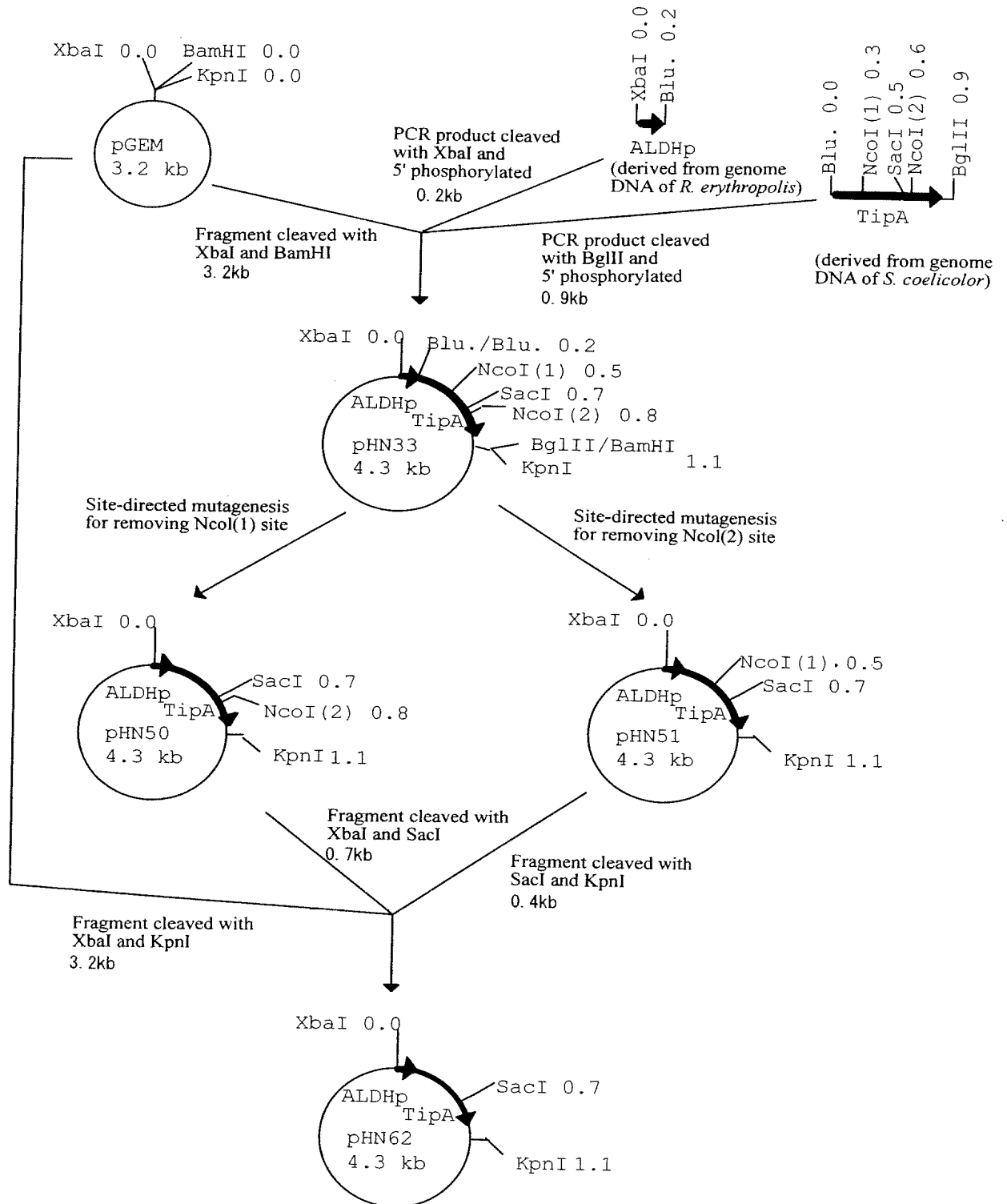


Fig. 4

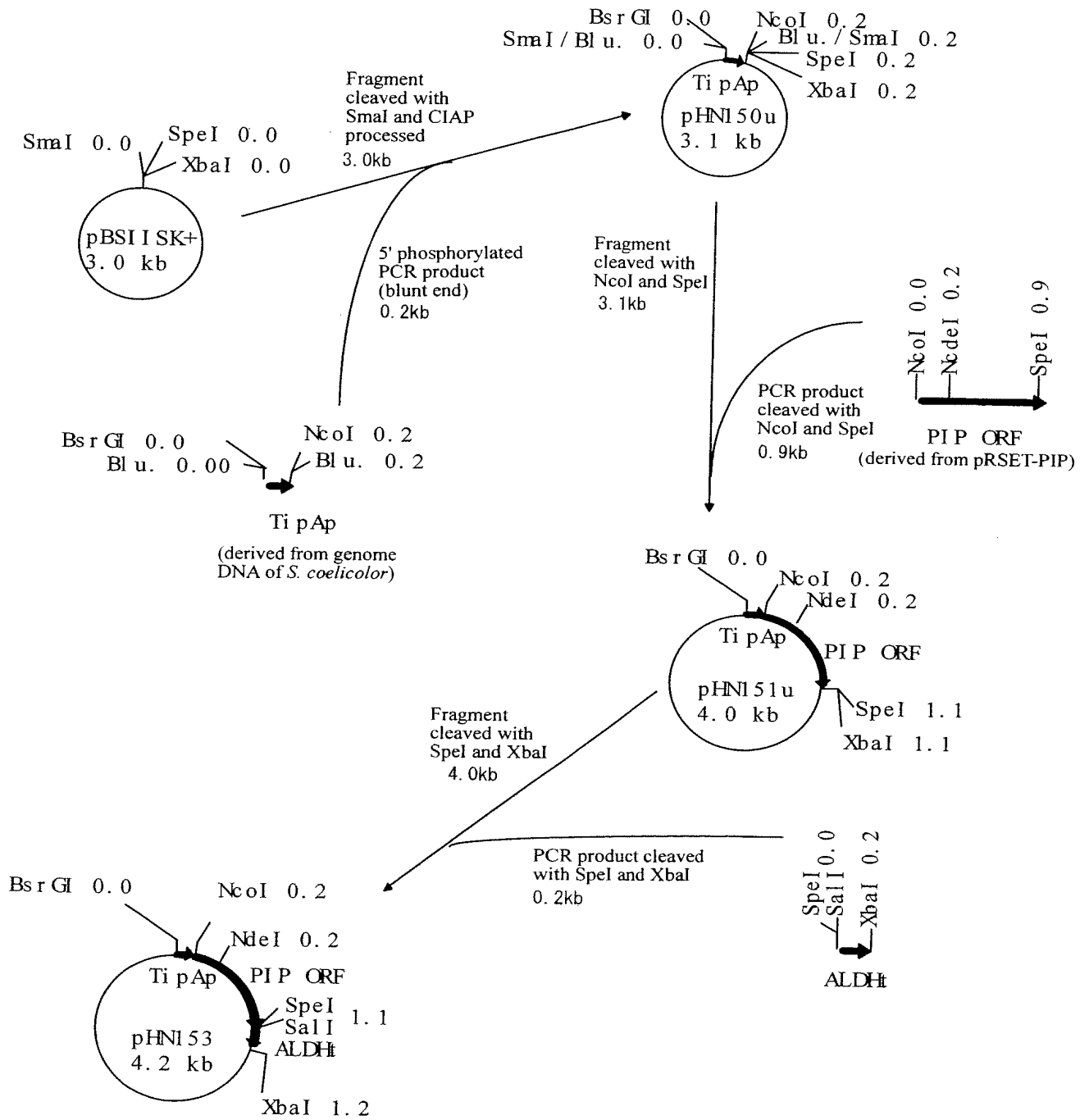


Fig. 5

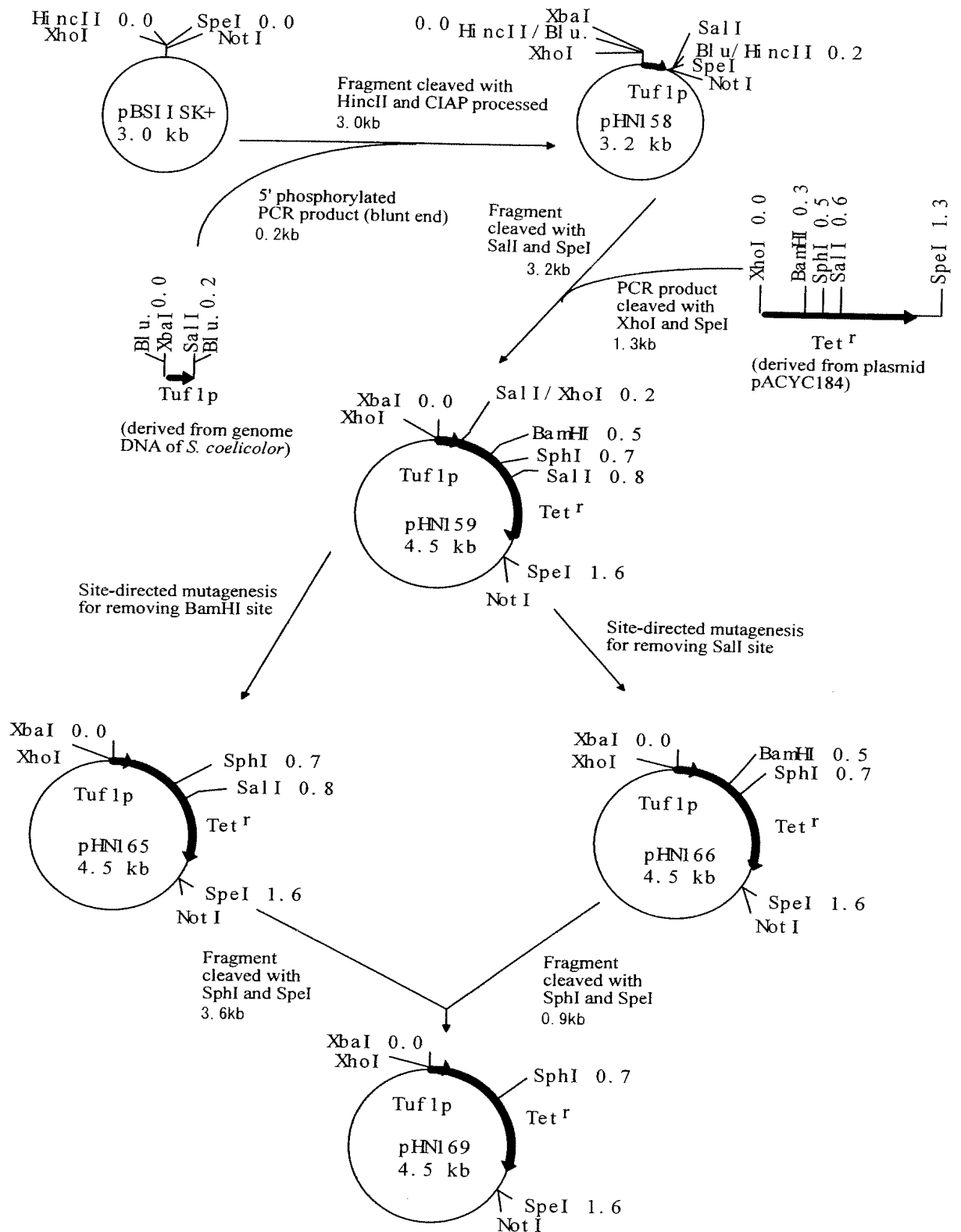


Fig. 6

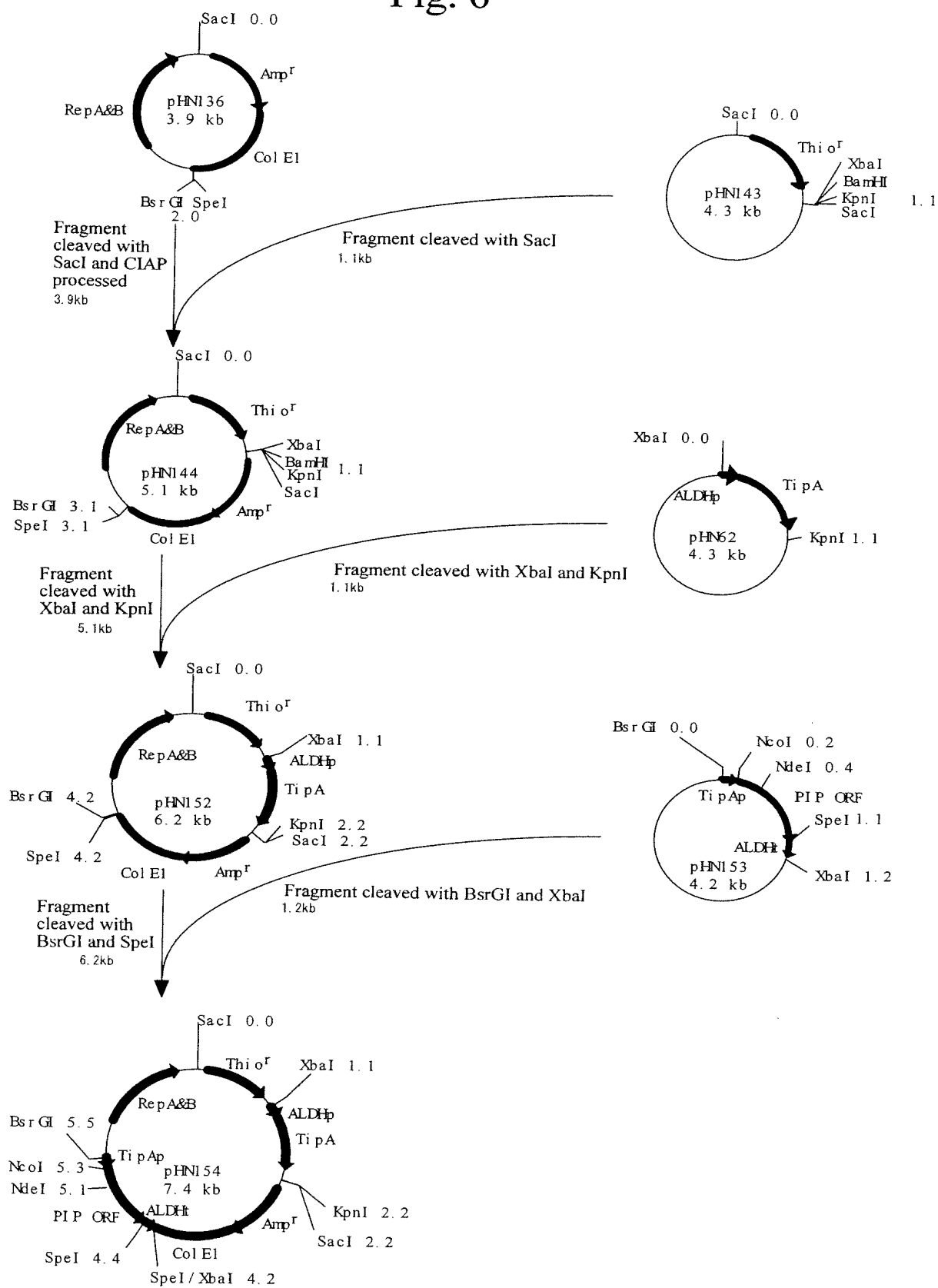


Fig. 6 (continued)

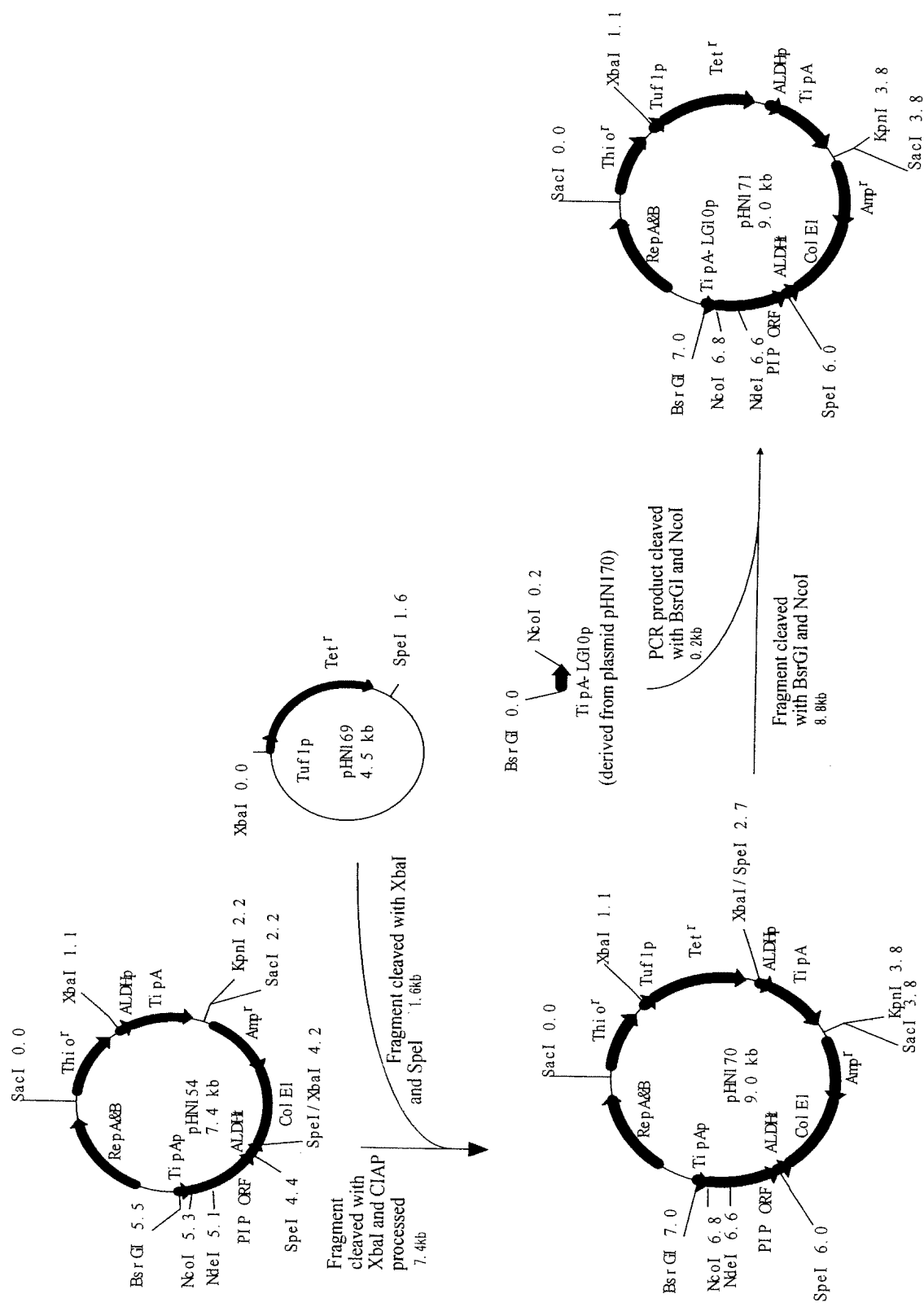


Fig. 7

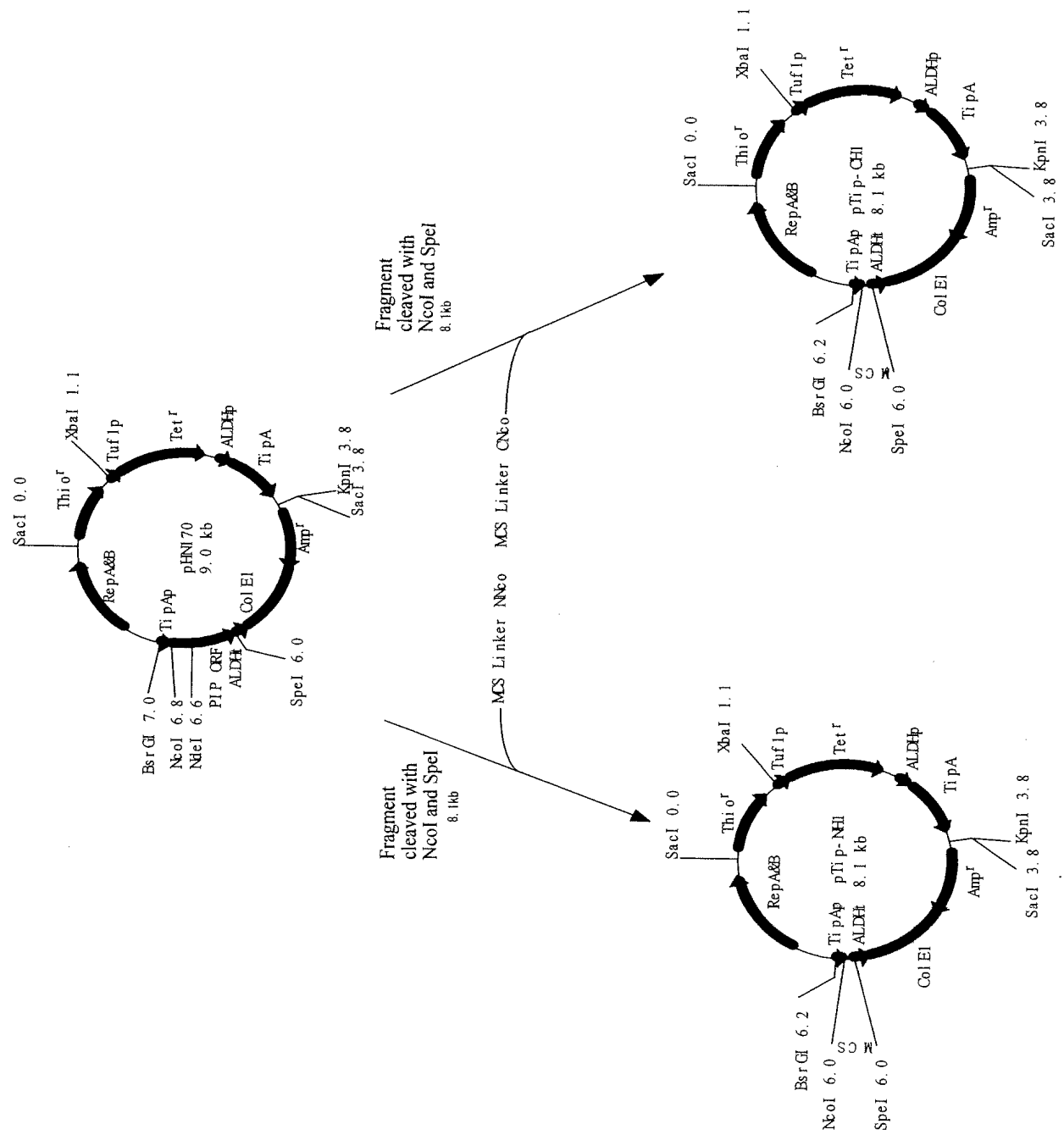




Fig. 7 (continued)

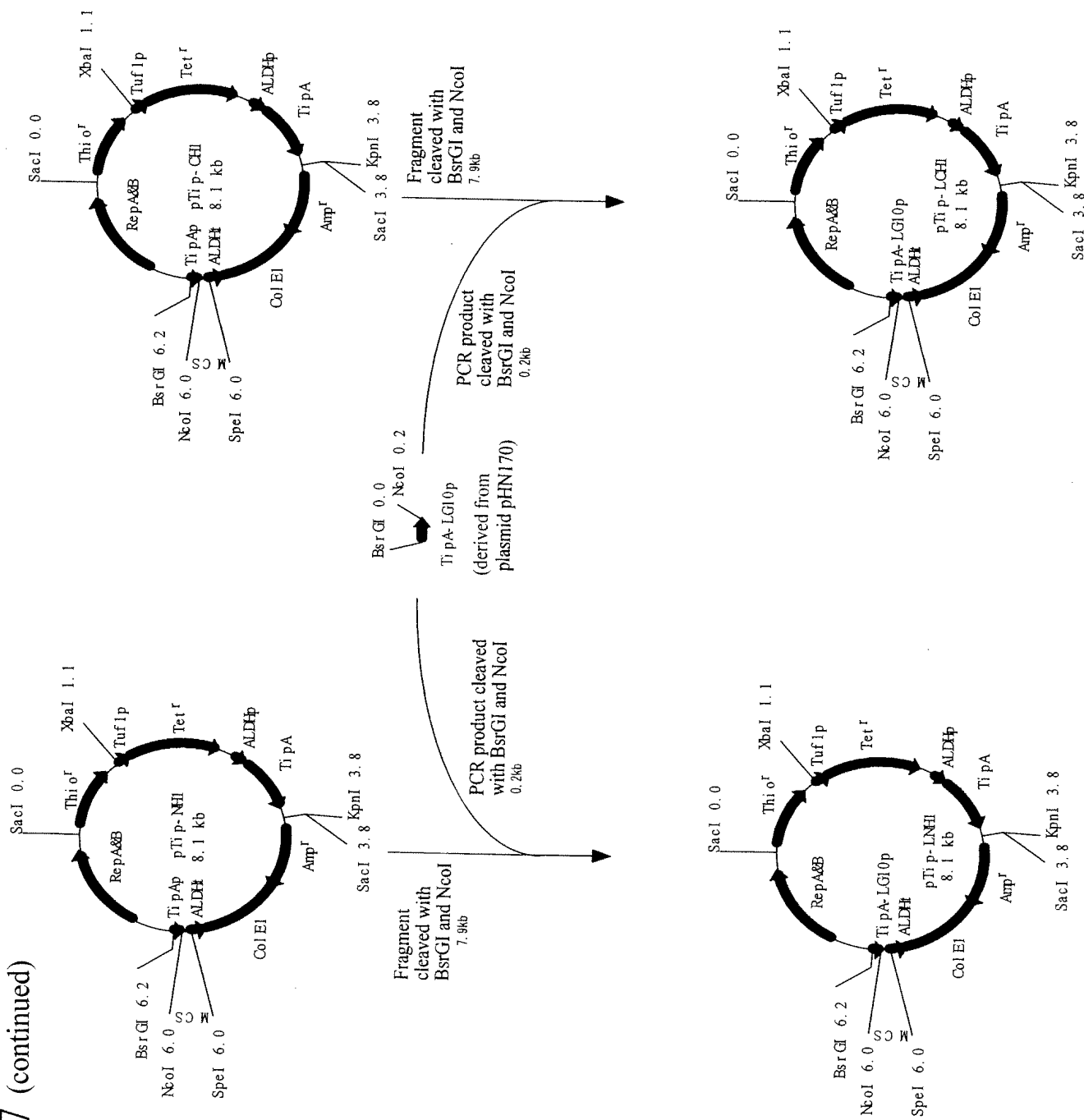


Fig. 8

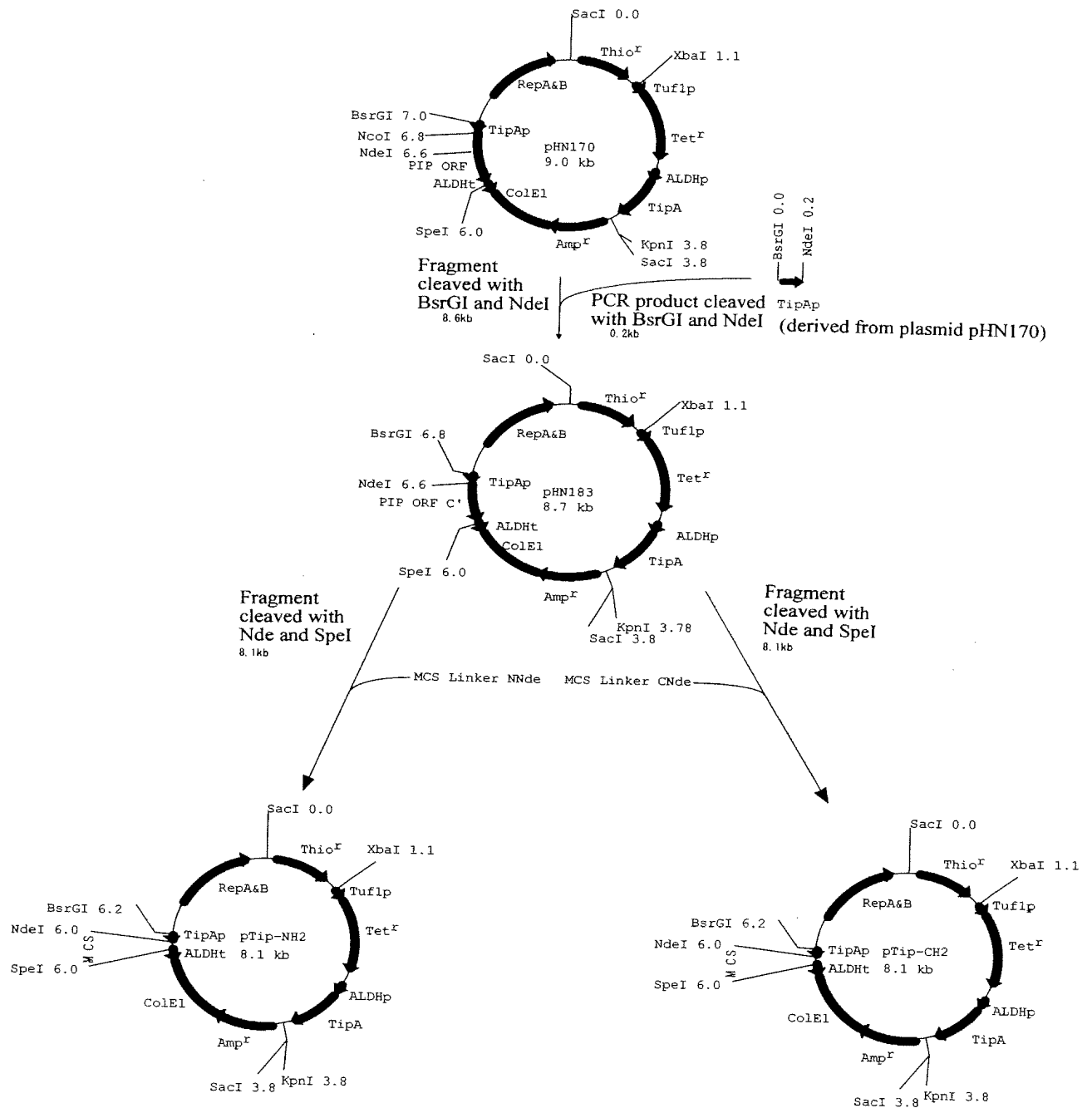


Fig. 8 (continued)

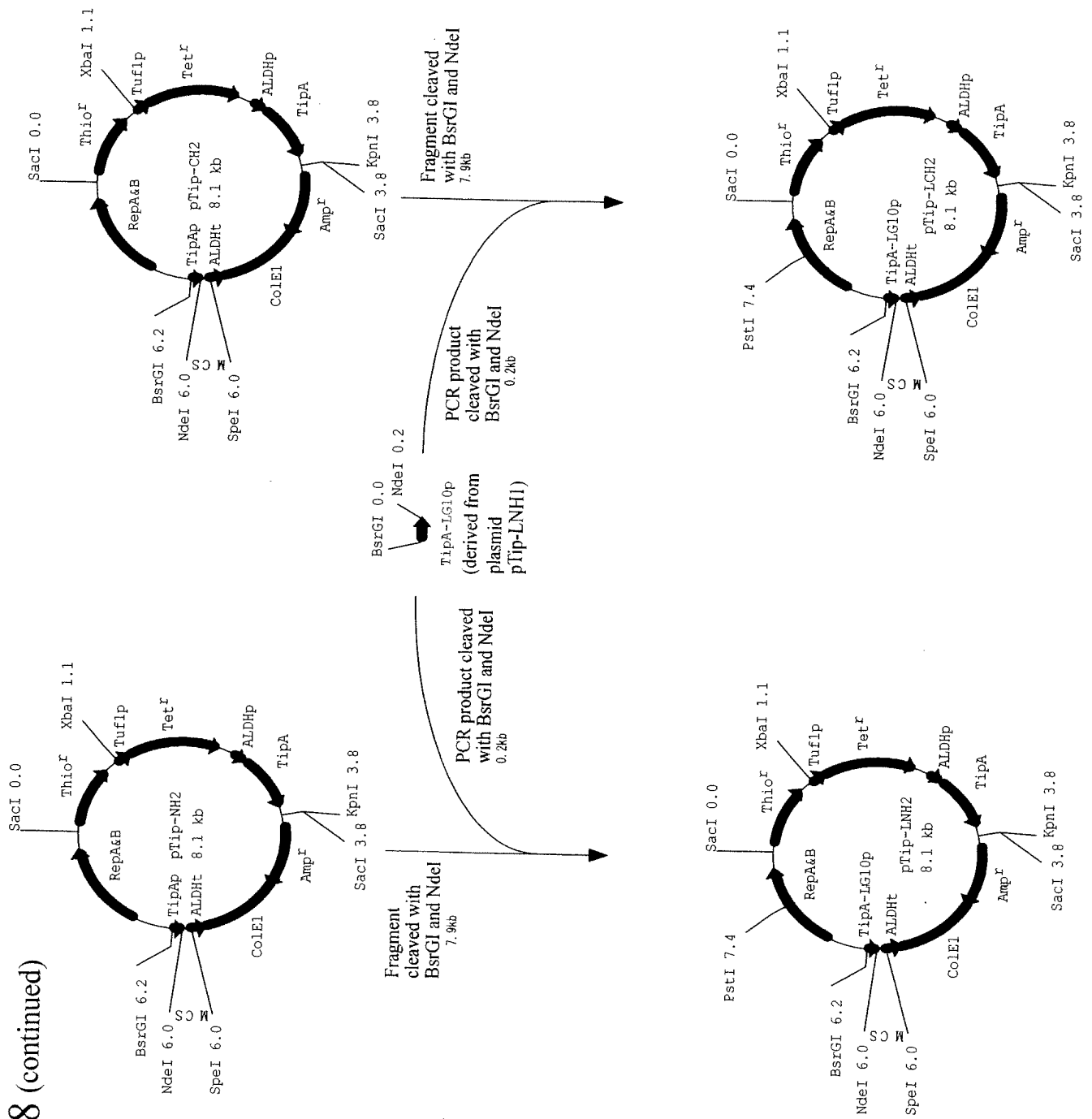
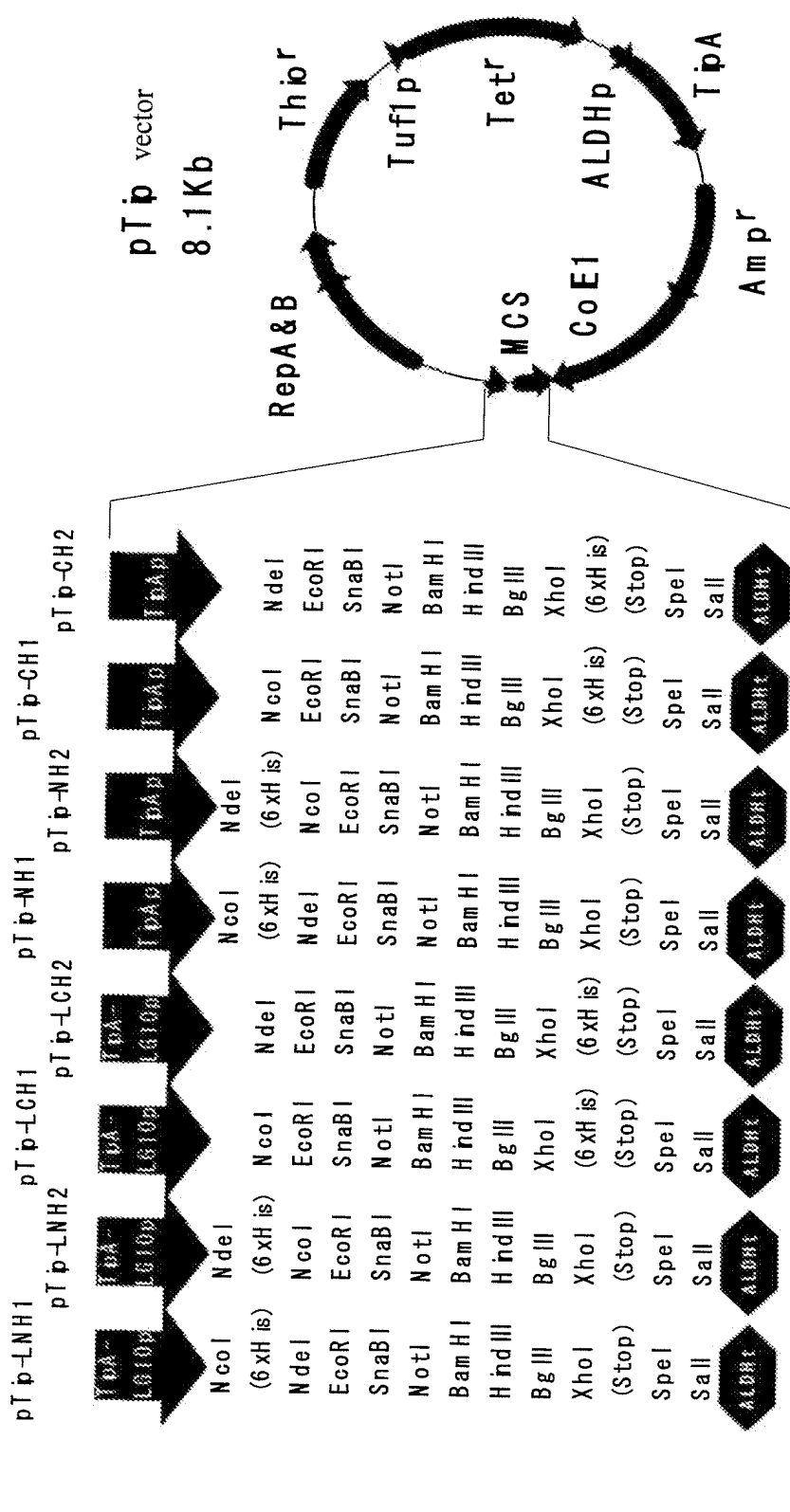


Fig. 9a



Thi<sup>r</sup> = confers thiostrepton resistance to *R. erythropolis*

ALDHp = promoter which constitutively produces TipA protein

TipA = encodes a TipA protein

TipAp = TipA promoter

TipA-LG10p = improved TipA promoter

ALDHt = transcription termination sequence

Regions necessary for the autonomous replication of a plasmid

CoIE1 = for *E. coli*

RepA&B = for *R. erythropolis*

Antibiotic resistance marker

Tuf1p-tet<sup>r</sup> = transformation marker for *R. erythropolis*

Amp<sup>r</sup> = transformation marker for *E. coli*

Fig. 9b

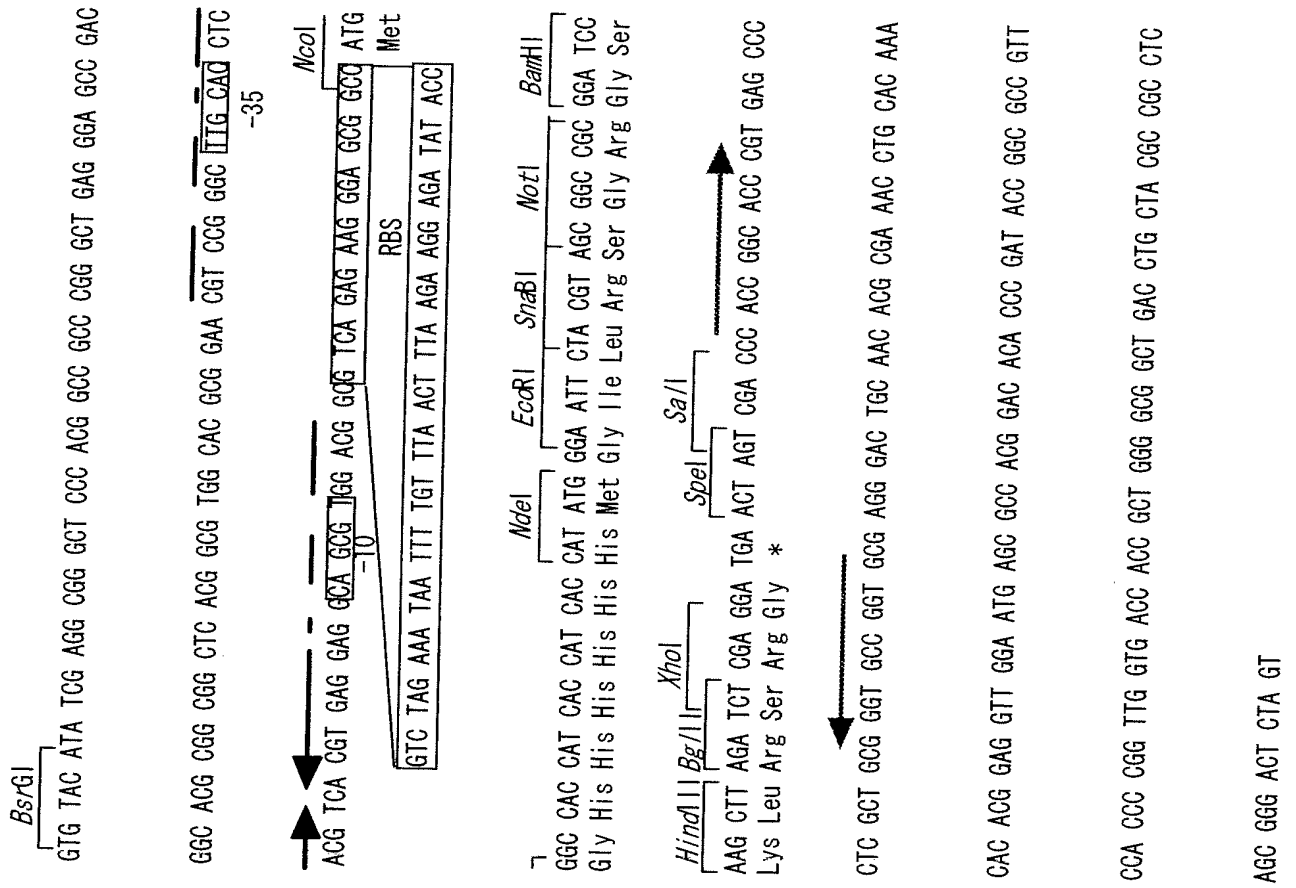


Fig. 9c

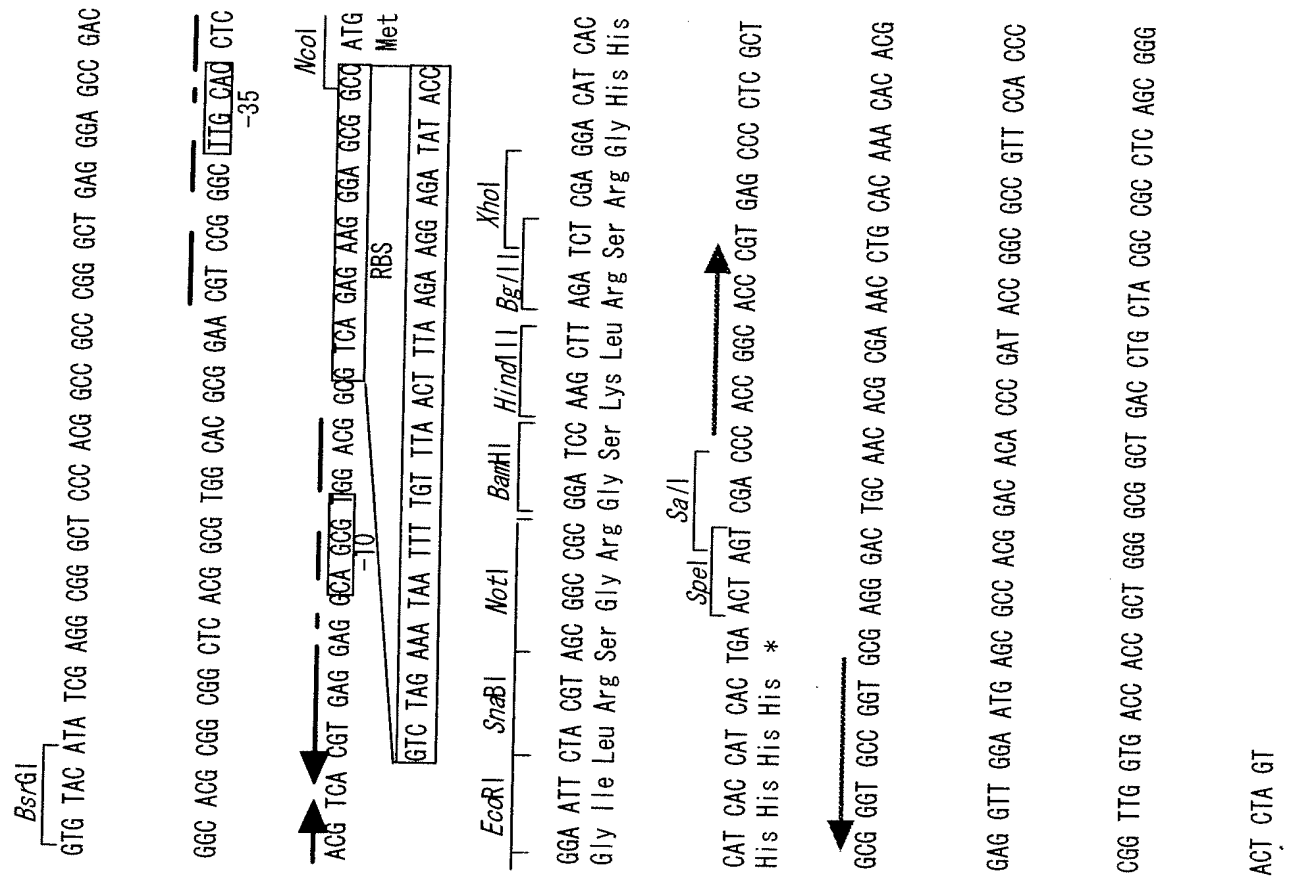


Fig. 9d

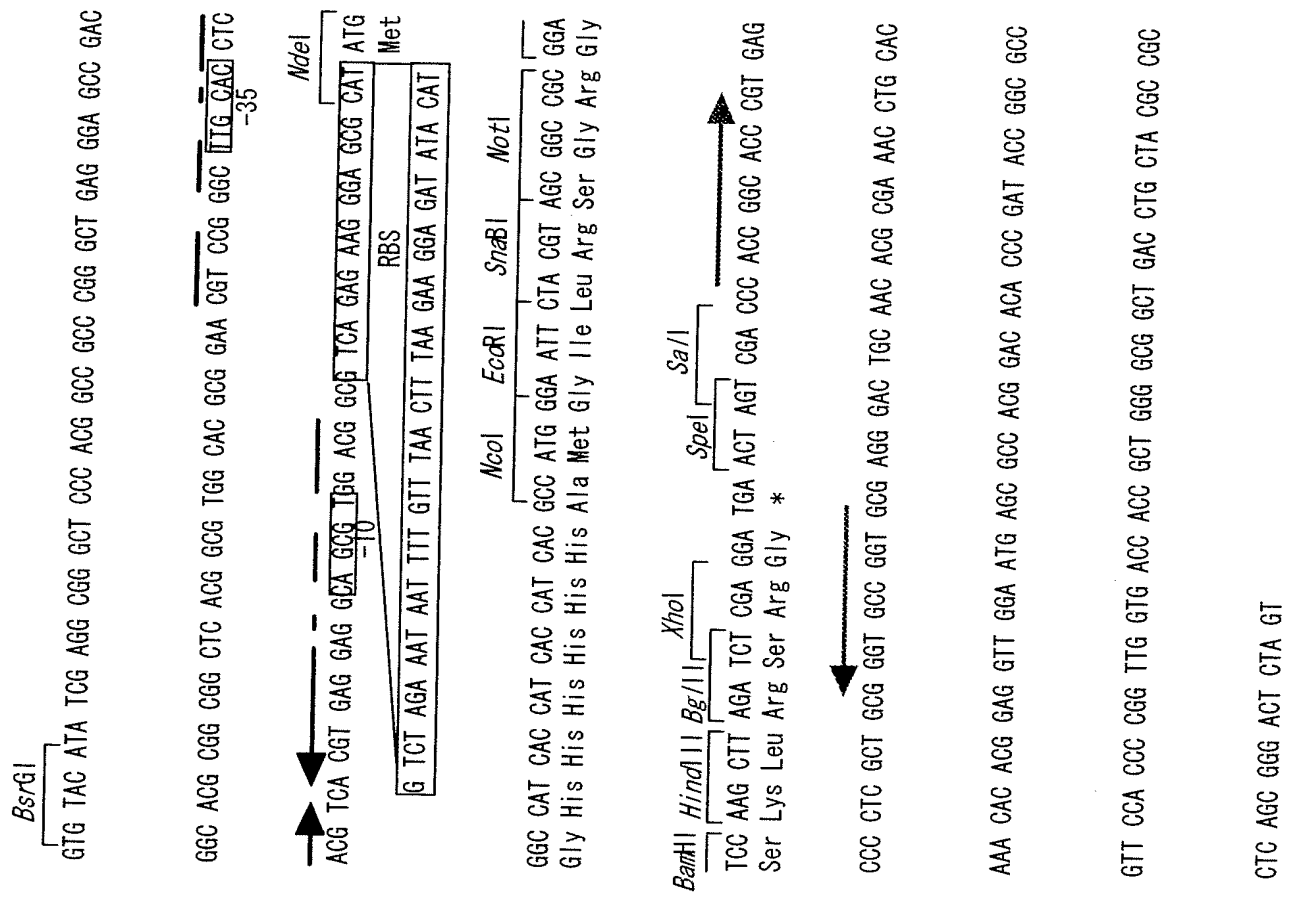
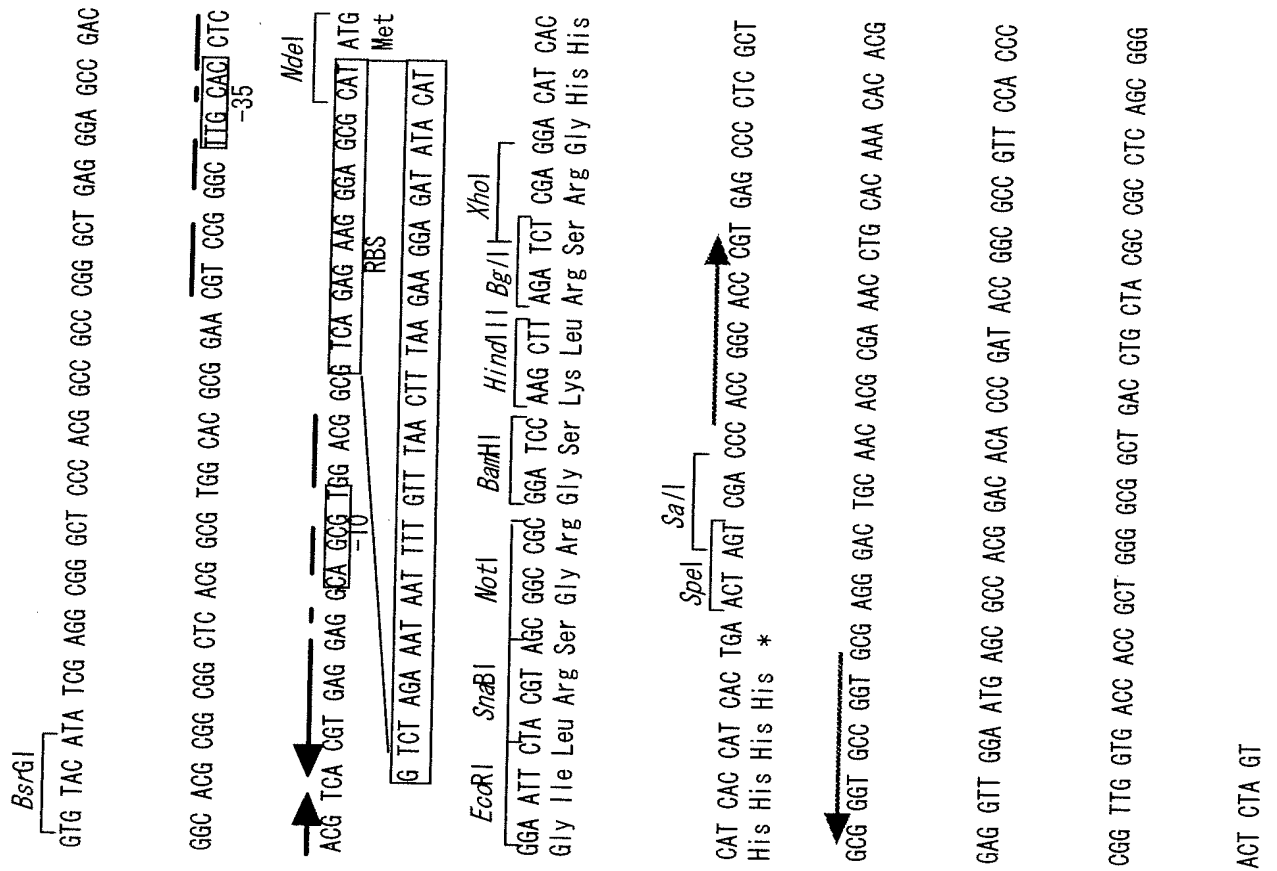


Fig. 9e





The diagram shows a circular plasmid map of pTip-CH1.1. The plasmid contains several key elements: RepA&B, Thio<sup>r</sup>, Tuf1p, Tet<sup>r</sup>, ALDHp, TipA, Amp<sup>r</sup>, CoE1, and MCS. A detailed view of the MCS region is provided below the map.

NcoI	EcoRI	SnaBI	NotI	BamHI	HindIII	BglII	XhoI
CC ATG GGA ATT CTA CGT AGC GGC CGC GGA TCC AAG CTT AGA TCT CTC GAG CAT CAC CAT CAC CAT CAC TGA ACT AGT CGA C							
Met Gly Ile Leu Arg Ser Gly Arg Gly Ser Lys Leu Arg Ser Leu Glu His His His His His *							

NdeI	EcoRI	SnaBI	NotI	BamHI	HindIII	BglII	XhoI
CAT ATG GGA ATT CTA CGT AGC GGC CGC GGA TCC AAG CTT AGA TCT CTC GAG CAT CAC CAT CAC CAT CAC TGA ACT AGT CGA C							
Met Gly Ile Leu Arg Ser Gly Arg Gly Ser Lys Leu Arg Ser Leu Glu His His His His His *							

Fig. 11

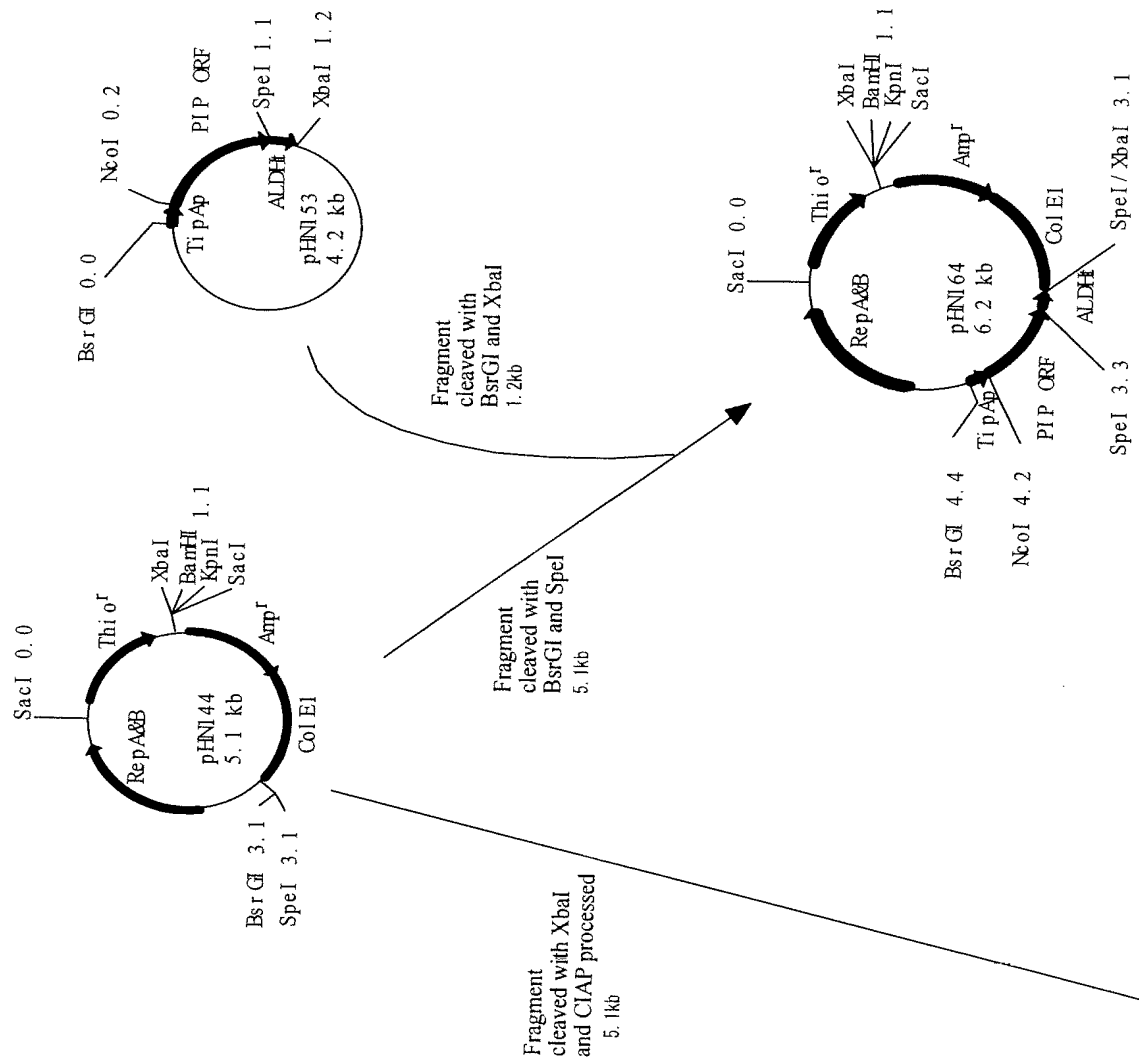


Fig. 11 (continued)

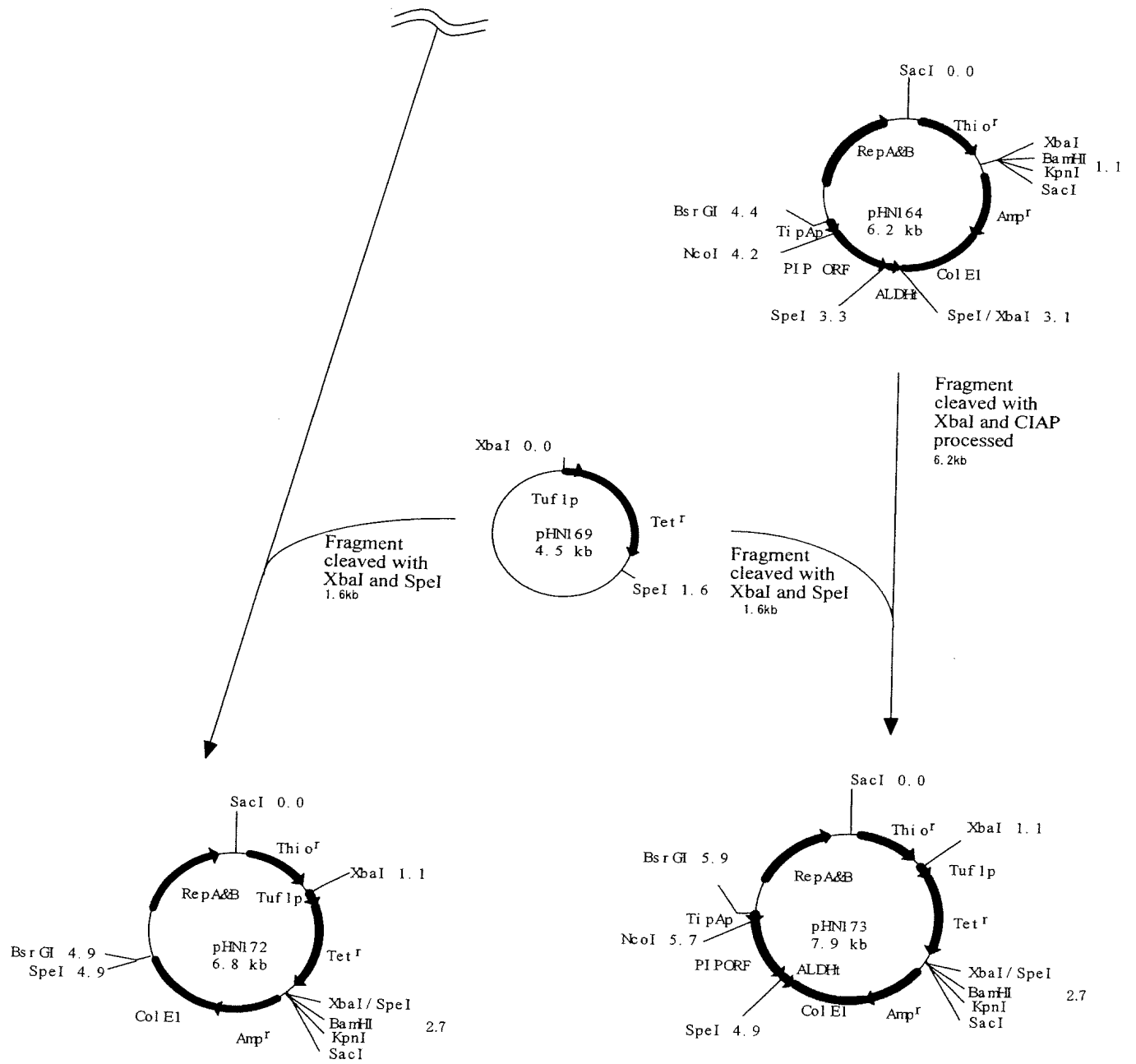


Fig. 12

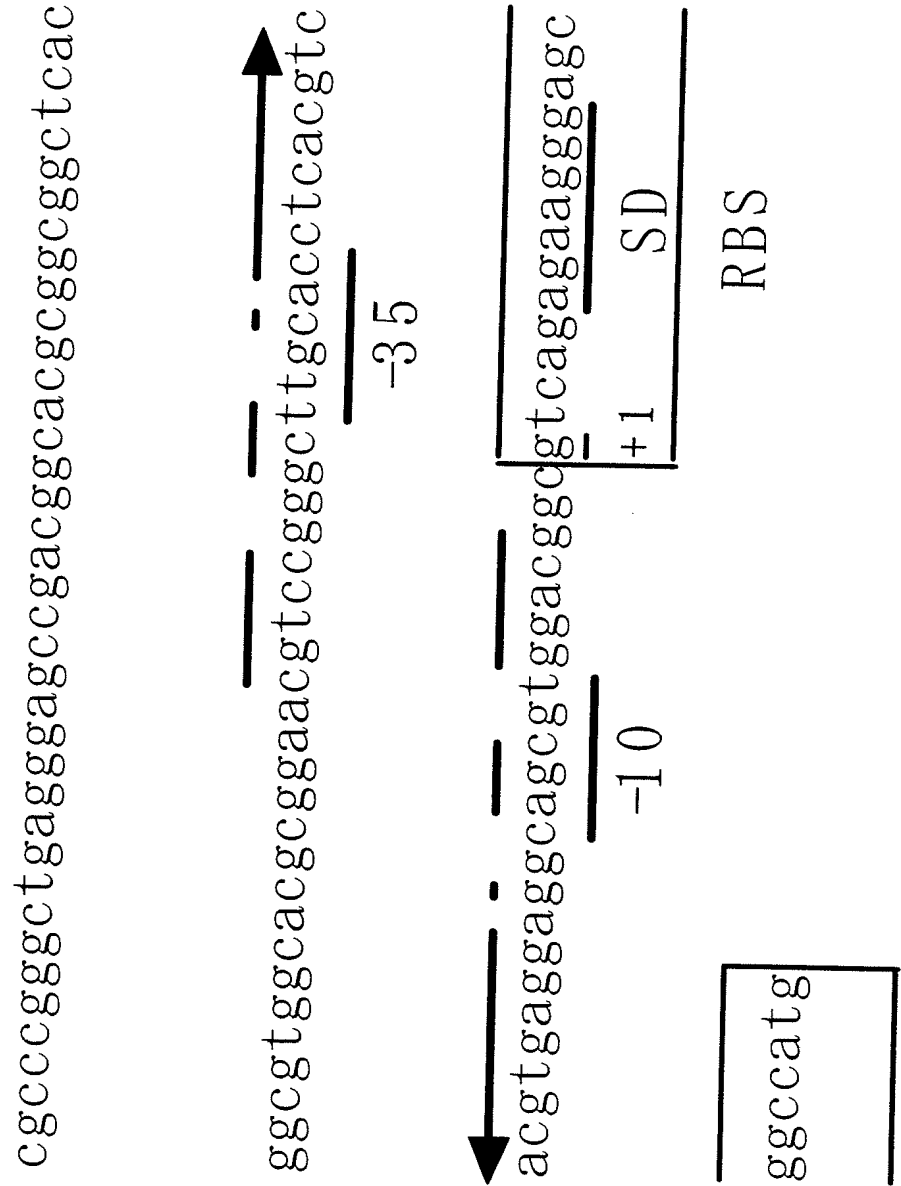


Fig. 13

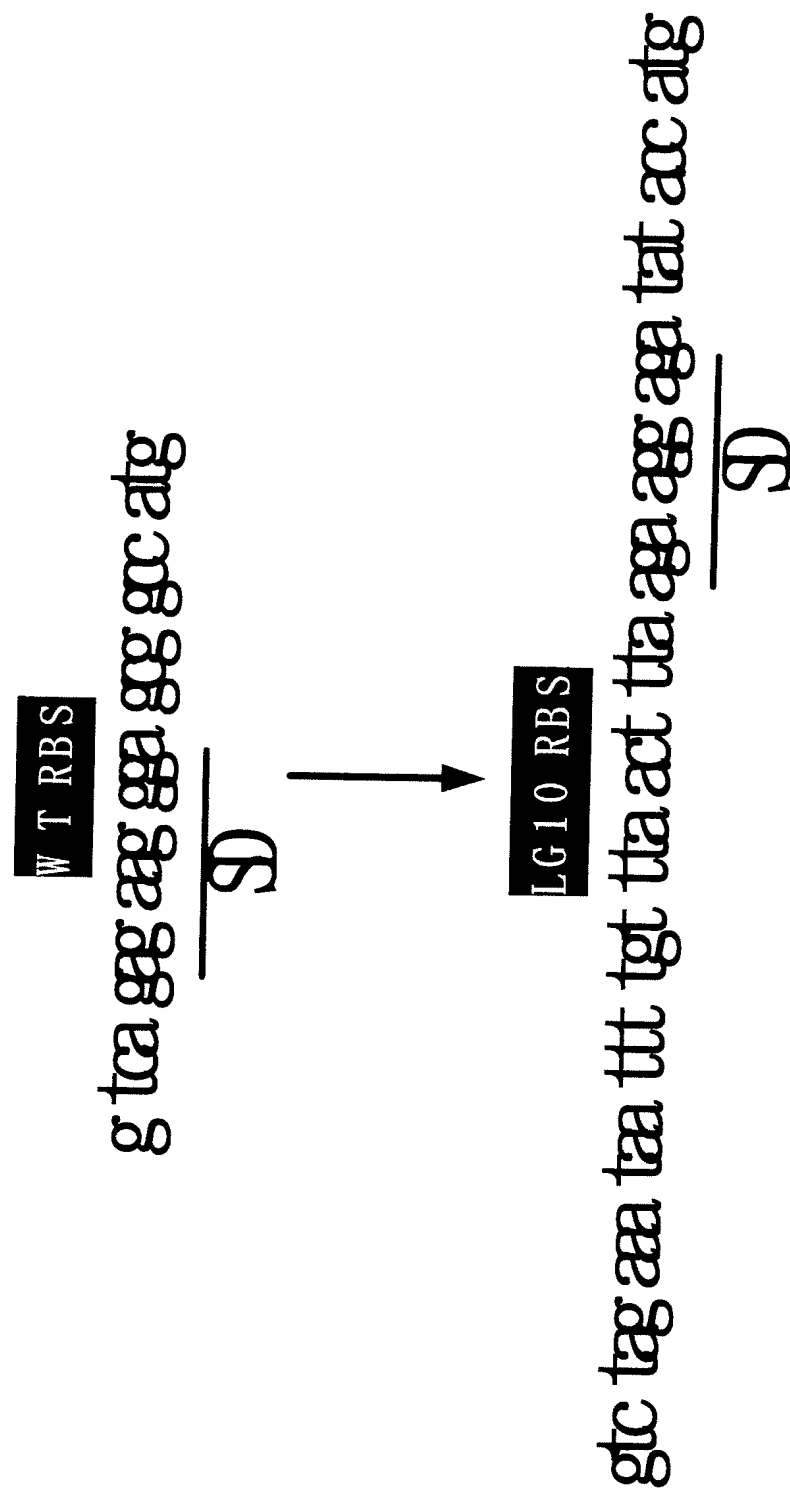


Fig. 14

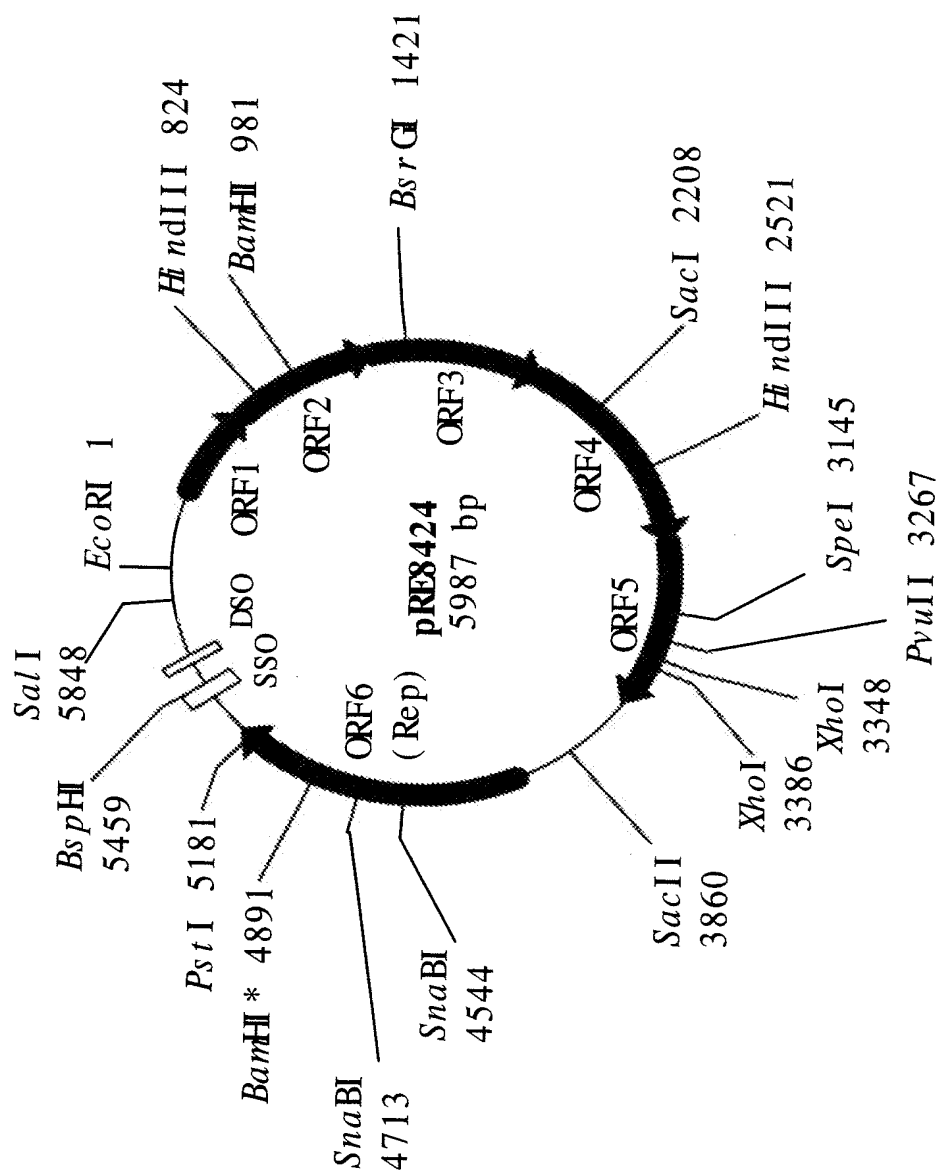


Fig. 15

	Motif IV	Motif I	Motif II	Motif III
Consensus	GLXXCGXXWCPXC	Xvt XTXRH	gXXgXXr aXe Xt XgXXn GwHXHXh Xi X	l aYYYYXXqX
pRE8424	68 GLRSCCKGW CPCC	26 MVTMTRH	33 GCDGYVRAVEI THCK-NGWHVHVHALL	53 LAAMLTKI AS
pAP1	138 GLHTCGSVWACPVC	27 MTLTQRH	33 GLVGYVRANEI THCK-HGWHVHSHVLI	67 I GNYVSKMQT
pBL1		76 MFVGTVRH	34 VEHYSDYEVTDS WA-NGWHLHRNMLL	54 MATYLAKGMS
pJV1	38 GLVRCCRI WF-CPEC	27 LVFTTARH	77 GYI GWRRAAEVTRS KKNGYHPHLNLLV	80 LIHMLTKNQD
pIJ101	20 GLMRCCRI WLC-PVC	27 LVFTTARH	59 GYVGM RATEVTVQQI NGWPHI HAI V	69 LAEYI AKTQD
pSN22	20 GLMRCCRI WLC-PVC	27 LVFTTARH	59 GYVGM RATEVTVQQI NGWPHI HAI V	69 LAEYI AKTQD
	** ** . * . * . *	: . . . * * *	: . . . . . . . . * . * . * . . . .	: . . . * . *
<b>C-terminal motif</b>				
Consensus	WKeyEXa XXgr Rai XWxr gl r			
pRE8424	276 WREFEFGSMGRRAI AWSRGLR			
pAP1	365 WKEYEKASFGRRALTWSKGLR			
pBL1	250 WREYEVGSKNLS-SWSRGAK			
pJV1	352 WAQYEEALAGRRAI EWTRGLR			
pIJ101	288 WHEYERATRGRAI EWTRYLR			
pSN22	288 WHEYERATKGRAI EWTRYLR			
	* : : * . * * : * : : :			

Fig. 16

pRE8424	5705	CGA <b>CCG</b> <b>GA</b> <b>AGCC</b> - <b>GA</b> - <b>CCCCCT</b> ----	<b>AGGTGGGGGAG</b> -
pAP1	2378	C <b>AGCT</b> <b>ATGC</b> - <b>C</b> - <b>GA</b> -AA <b>ACT</b> <b>TT</b> ----	<b>AGCA</b> <b>CAA</b> ----
pBL1	1314	GAA <b>ATA</b> <b>CAA</b> - <b>CTGA</b> - <b>ACACCT</b> <b>CTA</b> <b>AGCA</b> <b>ACCCGA</b> ----	
pJVI	3375	CTG <b>CC</b> <b>AAAA</b> <b>AGCGA</b> ----	<b>AGCTA</b> <b>AGGGTT</b>
pIJ101	1346	G <b>AGCC</b> <b>AAAA</b> - <b>CCGA</b> - <b>ACACCT</b> ----	<b>CCCA</b> <b>AGAAA</b> ----
pSN22	7805	G <b>ACCC</b> <b>AAAA</b> <b>CCCTCTC</b> <b>CCCCCT</b> ----	<b>CCCA</b> <b>AGAAA</b> ----

Nicking site

DSO



Fig. 17

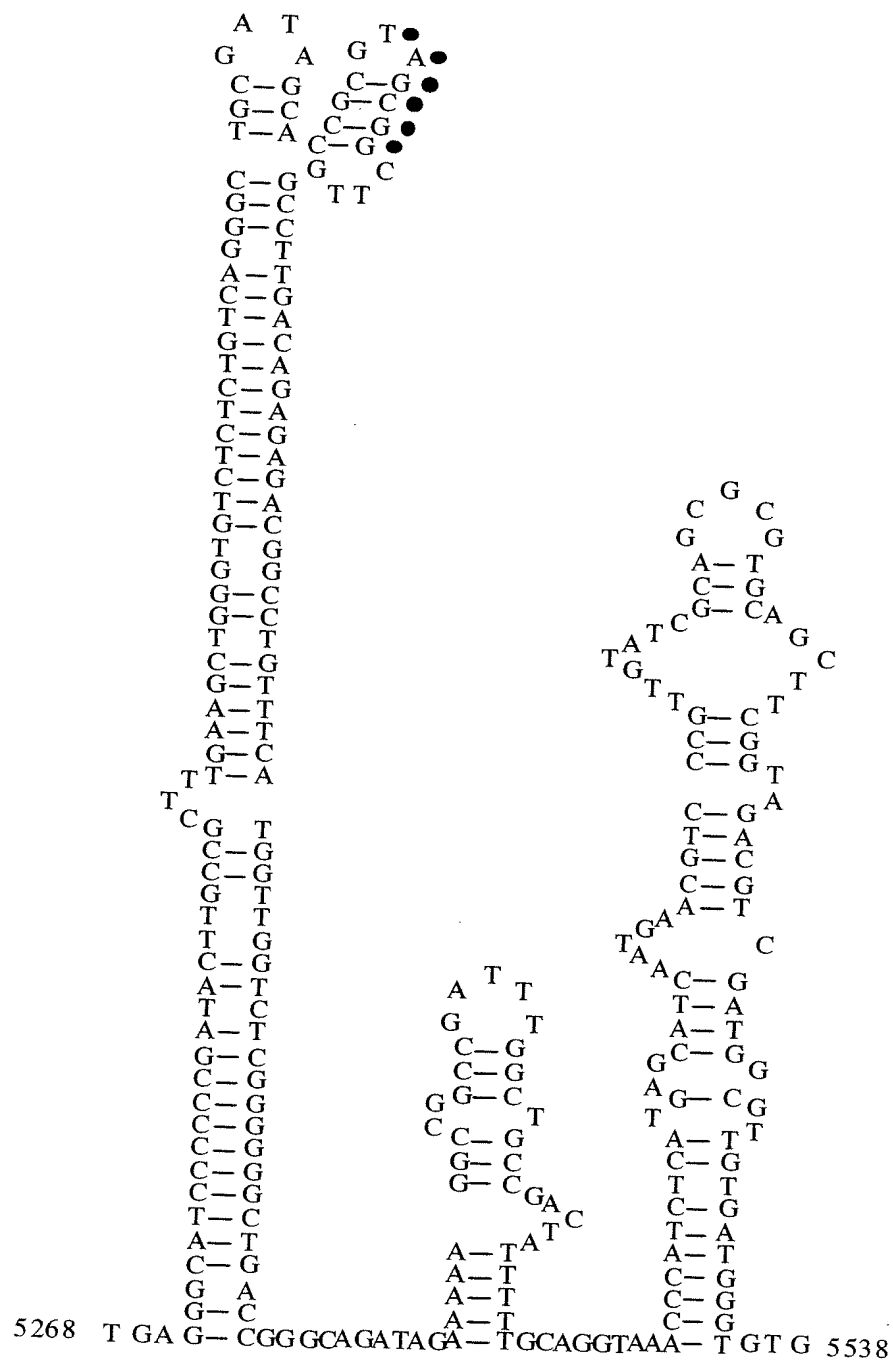


Fig. 18-1

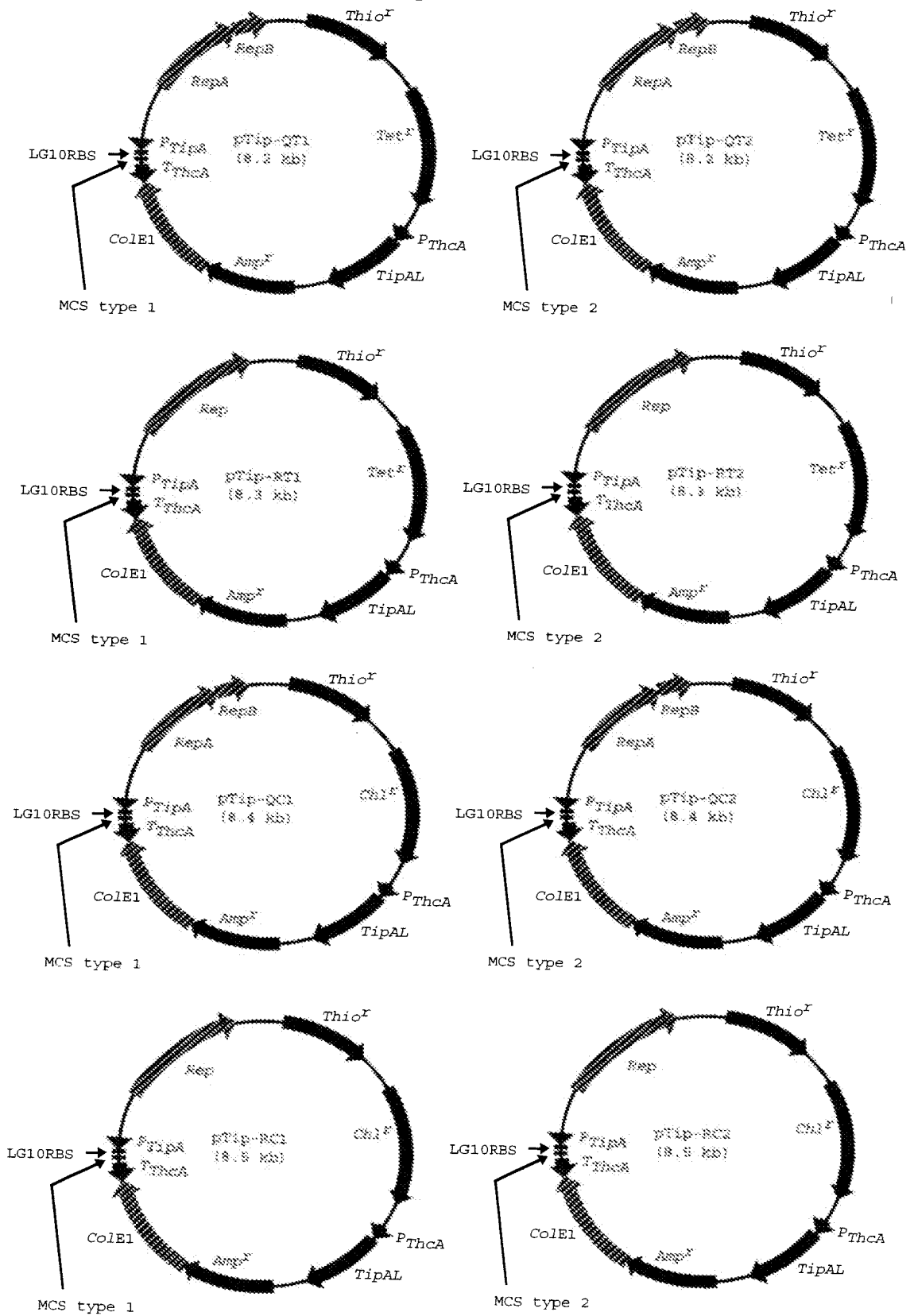


Fig. 18-2

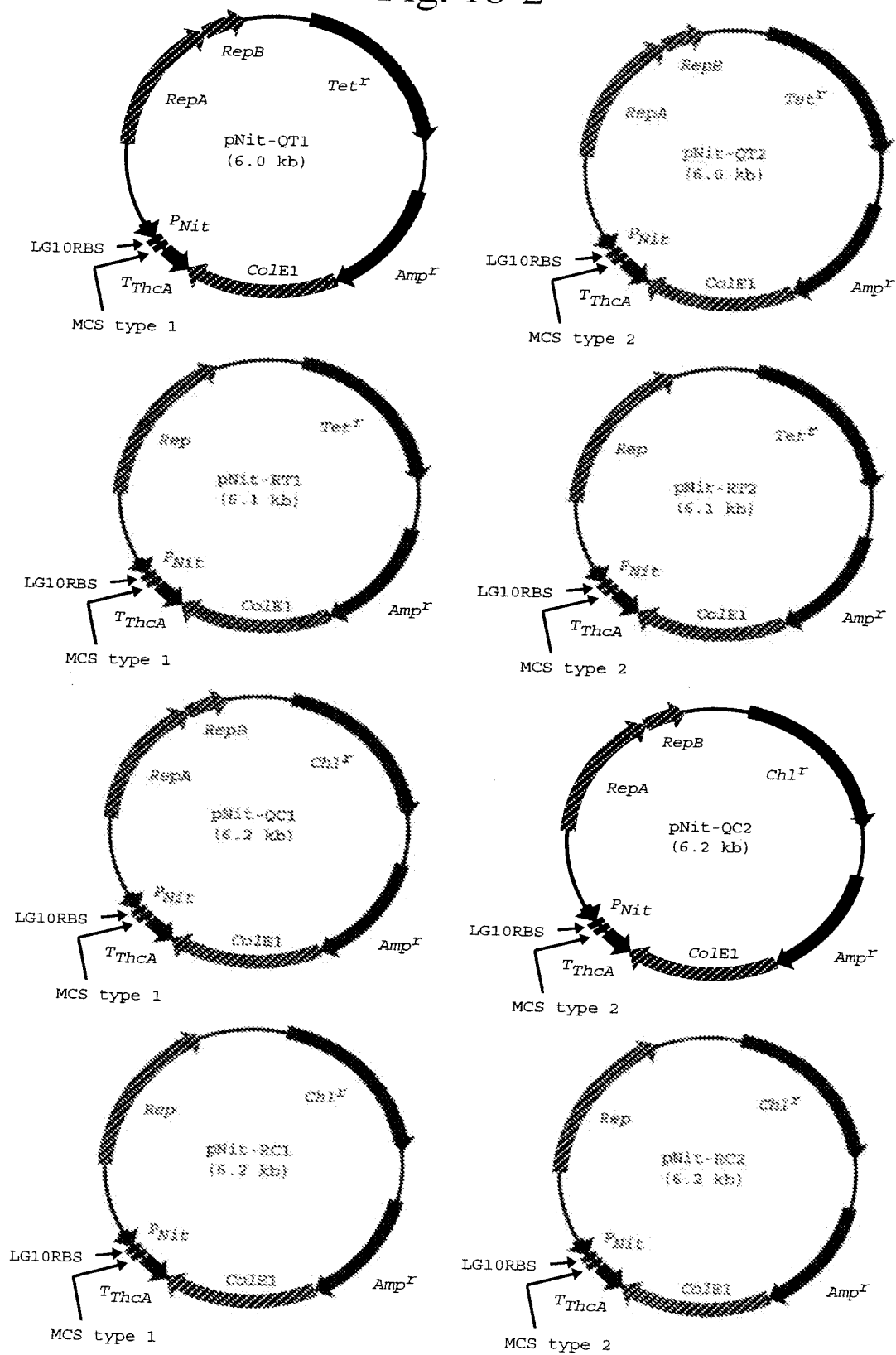




Fig. 20

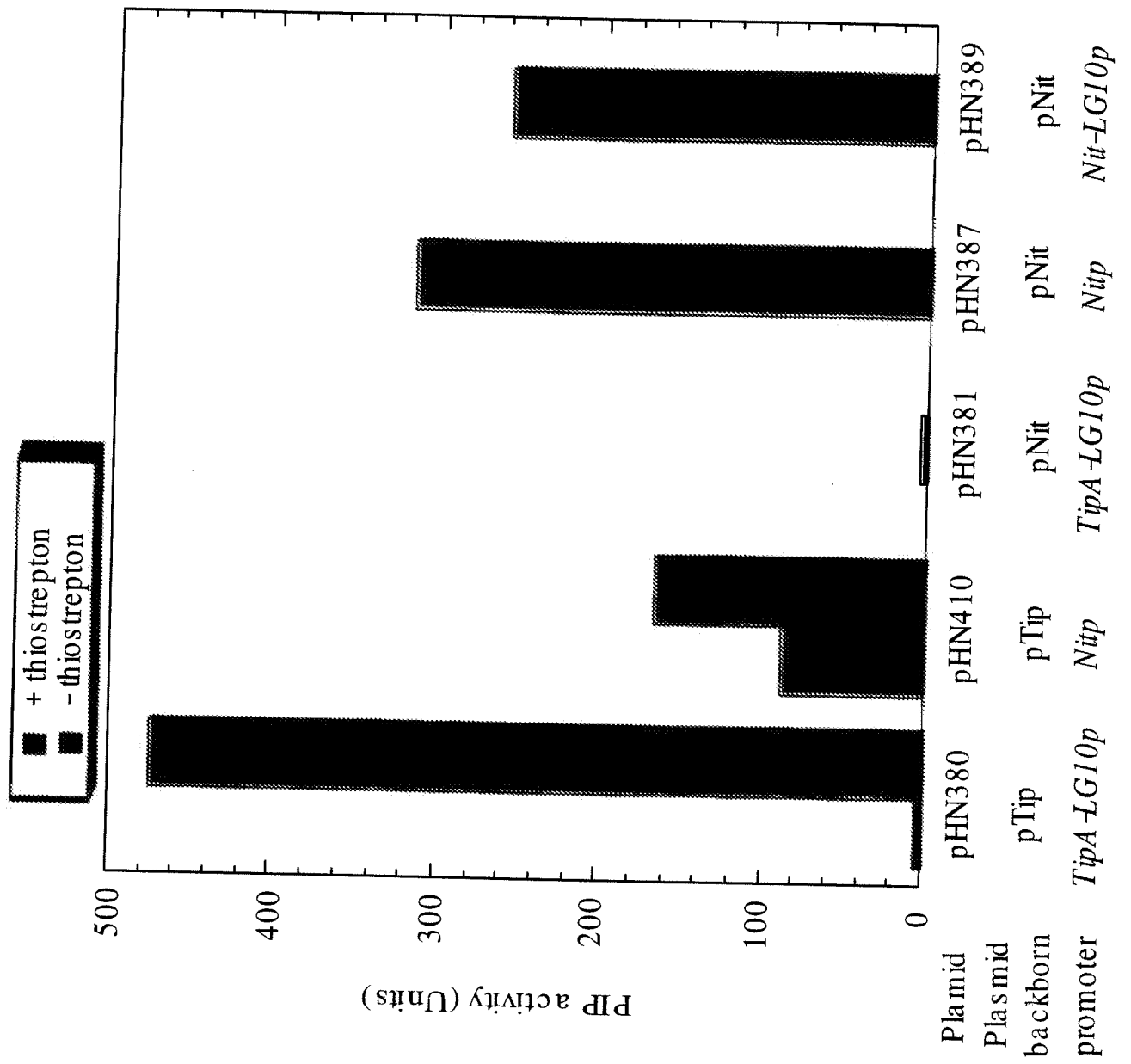


Fig. 21

